SEQUENCE LISTING

<110> Yano, Tetsuya; Nomoto, Tsuyoshi; Imamura, Takeshi; Canon Kabushiki Kaisha

<120> DNA Fragment Carrying Toluene Monooxygenase Gene, Recombinant Plasmid, Transformed Microorganism, Method for Degrading Chlorinated Aliphatic Hydrocarbon Compounds and Aromatic Compounds, and Method for Environmental Remediation

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<150> JP/

<151> 1998-10-30

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gcgaaattta acttcgcgtc agggctttcc ctgaattatc gagatttttt gctgcctggg 180

tcgaacgtgg cacggatgct gcattgaagt ccggcatgga ggcgacaccg atc         233
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atg aat cag cac ccc acc gat ctt tcc ccg ttc gat ccc ggc cgc aag   281
Met Asn Gln His Pro Thr Asp Leu Ser Pro Phe Asp Pro Gly Arg Lys
              5                  10                  15

tgc gtc cgc gtg acc ggc acg aac gcg cgc ggc ttc gtc gaa ttc gag   329
Cys Val Arg Val Thr Gly Thr Asn Ala Arg Gly Phe Val Glu Phe Glu
             20                  25                  30

ctg tcg atc ggc ggc gcg ccg gaa ctg tgc gtc gag ctg acg ttg tct   377
Leu Ser Ile Gly Gly Ala Pro Glu Leu Cys Val Glu Leu Thr Leu Ser
             35                  40                  45

cct gcc gcc ttc gat gcg ttc tgc cgc gaa cag cag gtc acg cgg ctc   425
Pro Ala Ala Phe Asp Ala Phe Cys Arg Glu Gln Gln Val Thr Arg Leu
             50                  55                  60

gac gtc gaa gcg aac cca                                            443
Asp Val Glu Ala Asn Pro
65                  70
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tgaccttgaggagcaagaa                                                462
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gtg acc atc gag ctg aag aca gtc gac atc aag ccg ctc cgg cac acc   510
Met Thr Ile Glu Leu Lys Thr Val Asp Ile Lys Pro Leu Arg His Thr
              5                  10                  15

ttt gcg cat gtc gcg cag aac atc ggc ggc gac aag acg gcg acg cgc   558
Phe Ala His Val Ala Gln Asn Ile Gly Gly Asp Lys Thr Ala Thr Arg
             20                  25                  30

tac cag gaa ggc atg atg ggc gcg cag ccc cag gag aac ttc cat tac   606
Tyr Gln Glu Gly Met Met Gly Ala Gln Pro Gln Glu Asn Phe His Tyr
             35                  40                  45

cgg ccg acc tgg gac ccg gac tac gag atc ttc gat ccg tcg cgc tcg   654
Arg Pro Thr Trp Asp Pro Asp Tyr Glu Ile Phe Asp Pro Ser Arg Ser
             50                  55                  60

gcg atc cgg atg gcg aac tgg tac gcg ttg aag gat ccg cgc cag ttc   702
Ala Ile Arg Met Ala Asn Trp Tyr Ala Leu Lys Asp Pro Arg Gln Phe
65                  70                  75                  80

tac tac gcg tcg tgg gcg acc acg cgg gcg cgc cag cag gat gcg atg   750
Tyr Tyr Ala Ser Trp Ala Thr Thr Arg Ala Arg Gln Gln Asp Ala Met
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                          85                    90                    95
gag tcg aac ttc gag ttc gtc gaa tcg cgc cgg atg atc ggc ctg atg    798
Glu Ser Asn Phe Glu Phe Val Glu Ser Arg Arg Met Ile Gly Leu Met
            100                   105                   110
cgc gac gac gtg gcc gcg cgg gcg ctc gac gtg ctg gtg ccg ctg cgc    846
Arg Asp Asp Val Ala Ala Arg Ala Leu Asp Val Leu Val Pro Leu Arg
            115                   120                   125
cac gcc gcg tgg ggc gcg aac atg aac aac gcg cag atc tgc gcg ctc    894
His Ala Ala Trp Gly Ala Asn Met Asn Asn Ala Gln Ile Cys Ala Leu
        130                   135                   140
ggc tac ggc acg gtg ttc acc gcg ccc gcg atg ttc cat gcg atg gac    942
Gly Tyr Gly Thr Val Phe Thr Ala Pro Ala Met Phe His Ala Met Asp
145                   150                   155                   160
aac ctc ggc gtc gcg caa tac ctc acg cgt ctc gcg ctc gcg atg gcc    990
Asn Leu Gly Val Ala Gln Tyr Leu Thr Arg Leu Ala Leu Ala Met Ala
                  165                   170                   175
gag ccc gac gtg ctg gag gcg gcc aag gcg acc tgg acc cgc gac gcc   1038
Glu Pro Asp Val Leu Glu Ala Ala Lys Ala Thr Trp Thr Arg Asp Ala
            180                   185                   190
gcc tgg cag ccg ctg cgc cgc tac gtc gag gac acg ctg gtc gtc gcc   1086
Ala Trp Gln Pro Leu Arg Arg Tyr Val Glu Asp Thr Leu Val Val Ala
            195                   200                   205
gat ccg gtc gag ctg ttc atc gcg cag aac ctc gcg ctc gac ggc ctg   1134
Asp Pro Val Glu Leu Phe Ile Ala Gln Asn Leu Ala Leu Asp Gly Leu
        210                   215                   220
ctg tat ccg ctc gtc tac gac cgc ttc gtc gac gaa cgg atc gcg ctc   1182
Leu Tyr Pro Leu Val Tyr Asp Arg Phe Val Asp Glu Arg Ile Ala Leu
225                   230                   235                   240
gaa ggc ggc tcg gca gtc gcg atg ctg acc gcg ttc atg ccc gaa tgg   1230
Glu Gly Gly Ser Ala Val Ala Met Leu Thr Ala Phe Met Pro Glu Trp
                  245                   250                   255
cac acc gag tcg aac cgc tgg atc gac gcg gtc gtg aag acg atg gcc   1278
His Thr Glu Ser Asn Arg Trp Ile Asp Ala Val Val Lys Thr Met Ala
            260                   265                   270
gcc gaa tcc gac gac aac cgc gcg ctg ctc gcc cgc tgg aca cgc gac   1326
Ala Glu Ser Asp Asp Asn Arg Ala Leu Leu Ala Arg Trp Thr Arg Asp
        275                   280                   285
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tgg tcc gcg cgc gcc gag gcg gca ctg gca ccg gtg gcg gca cgc gcg   1374
Trp Ser Ala Arg Ala Glu Ala Ala Leu Ala Pro Val Ala Ala Arg Ala
     290   295   300

ctg cag gat gcc ggg cgc gcg gcg ctc gac gaa gtg cgc gag cag ttc   1422
Leu Gln Asp Ala Gly Arg Ala Ala Leu Asp Glu Val Arg Glu Gln Phe
305   310   315   320

cac gca cgc gcg gcc agg ctc ggc atc gcg ctc   1455
His Ala Arg Ala Ala Arg Leu Gly Ile Ala Leu
        325   330

tgacgacggg aatcctccct taacccaagg aatgccagc   1494

atg tcc aac gta ttc atc gcc ttt cag gcc aat gag gac tcc aga ccg   1542
Met Ser Asn Val Phe Ile Ala Phe Gln Ala Asn Glu Asp Ser Arg Pro
         5   10   15

atc gtg gat gcg atc gtc gcc gac aac ccg cgc gcg gtg gtg gtc gag   1590
Ile Val Asp Ala Ile Val Ala Asp Asn Pro Arg Ala Val Val Val Glu
        20   25   30

tcg ccc ggc atg gtc aag atc gac gcg ccg gac cgg ctg acg atc cgc   1638
Ser Pro Gly Met Val Lys Ile Asp Ala Pro Asp Arg Leu Thr Ile Arg
        35   40   45

cgc gaa acg atc gag gaa ctg acc ggc acg cgc ttc gac ctg cag cag   1686
Arg Glu Thr Ile Glu Glu Leu Thr Gly Thr Arg Phe Asp Leu Gln Gln
        50   55   60

ctc cag gtc aac ctg atc acg ctg tca ggc cac atc gac gag gac gac   1734
Leu Gln Val Asn Leu Ile Thr Leu Ser Gly His Ile Asp Glu Asp Asp
65   70   75   80

gac gag ttc acg ctg agc tgg tcg cac   1761
Asp Glu Phe Thr Leu Ser Trp Ser His
        85

tgaacgccgc gccacgcgca ccgacaacac cggagacacg a   1802

atg gac acg cca acg ctc aag aaa aaa ctc ggc ctg aag gac cgc tac   1850
Met Asp Thr Pro Thr Leu Lys Lys Lys Leu Gly Leu Lys Asp Arg Tyr
         5   10   15

gcg gca atg acg cgc ggc ctc ggc tgg gag acg acc tac cag ccg atg   1898
Ala Ala Met Thr Arg Gly Leu Gly Trp Glu Thr Thr Tyr Gln Pro Met
        20   25   30

gac aag gtc ttc ccg tac gac cgc tac gag ggc atc aag atc cac gac   1946
Asp Lys Val Phe Pro Tyr Asp Arg Tyr Glu Gly Ile Lys Ile His Asp

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              35                    40                    45
tgg gac aag tgg gtc gac ccg ttc cgc ctg acg atg gat gcg tac tgg   1994
Trp Asp Lys Trp Val Asp Pro Phe Arg Leu Thr Met Asp Ala Tyr Trp
         50                    55                    60
aaa tac cag ggc gag aag gaa aag aag ctg tac gcg gtg atc gac gcg   2042
Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu Tyr Ala Val Ile Asp Ala
 65                    70                    75                    80
ttc acg cag aac aac gcg ttc ctc ggc gtg agc gac gcc cgc tac atc   2090
Phe Thr Gln Asn Asn Ala Phe Leu Gly Val Ser Asp Ala Arg Tyr Ile
              85                    90                    95
aac gcg ctg aag ctg ttc ctc cag ggc gtg acg ccg ctc gaa tac ctc   2138
Asn Ala Leu Lys Leu Phe Leu Gln Gly Val Thr Pro Leu Glu Tyr Leu
             100                   105                   110
gcg cac cgc ggc ttc gcg cat gtc ggc cgg cac ttc acc ggc gag ggc   2186
Ala His Arg Gly Phe Ala His Val Gly Arg His Phe Thr Gly Glu Gly
             115                   120                   125
gcg cgc atc gcg tgc cag atg cag tcg atc gac gag ctg cgg cac tac   2234
Ala Arg Ile Ala Cys Gln Met Gln Ser Ile Asp Glu Leu Arg His Tyr
         130                   135                   140
cag acc gaa acg cat gcg atg tcg acg tac aac aag ttc ttc aac ggg   2282
Gln Thr Glu Thr His Ala Met Ser Thr Tyr Asn Lys Phe Phe Asn Gly
 145                   150                   155                   160
ttc cat cac tcg aac cag tgg ttc gac cgc gtg tgg tac ctg tcg gtg   2330
Phe His His Ser Asn Gln Trp Phe Asp Arg Val Trp Tyr Leu Ser Val
                  165                   170                   175
ccg aag tcg ttc ttc gag gac gcg tat tcg tcg ggg ccg ttc gag ttc   2378
Pro Lys Ser Phe Phe Glu Asp Ala Tyr Ser Ser Gly Pro Phe Glu Phe
              180                   185                   190
ctg acc gcg gtc agc ttc tcg ttc gaa tac gtg ctg acg aac ctg ctg   2426
Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu
              195                   200                   205
ttc gtg ccg ttc atg tcg ggc gcc gcc tac aac ggt gac atg tcg acc   2474
Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr
         210                   215                   220
gtc acg ttc ggc ttc tcc gcg cag tcg gac gaa tcg cgt cac atg acg   2522
Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr
 225                   230                   235                   240
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ctc ggc atc gaa tgc atc aag ttc ctg ctc gaa cag gac ccg gac aac 2570
Leu Gly Ile Glu Cys Ile Lys Phe Leu Leu Glu Gln Asp Pro Asp Asn
                245   250   255

gtg ccg atc gtg cag cgc tgg atc gac aag tgg ttc tgg cgc ggc tac 2618
Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr
            260   265   270

cgg ctg ctg acg ctg gtc gcg atg atg atg gac tac atg cag ccc aag 2666
Arg Leu Leu Thr Leu Val Ala Met Met Met Asp Tyr Met Gln Pro Lys
            275   280   285

cgc gtg atg agc tgg cgc gag tcg tgg gag atg tac gcc gag cag aac 2714
Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Ala Glu Gln Asn
            290   295   300

ggc ggc gcg ctg ttc aag gat ctc gcg cgc tac ggc att cgc gag ccg 2762
Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg Tyr Gly Ile Arg Glu Pro
305   310   315   320

aag ggc tgg cag gac gcc tgc gaa ggc aag gat cac atc agc cac cag 2810
Lys Gly Trp Gln Asp Ala Cys Glu Gly Lys Asp His Ile Ser His Gln
            325   330   335

gcg tgg tcg acg ttc tac ggc ttc aac gcg gcc tcg gcg ttc cac acc 2858
Ala Trp Ser Thr Phe Tyr Gly Phe Asn Ala Ala Ser Ala Phe His Thr
            340   345   350

tgg gtg ccg acc gaa gac gaa atg ggc tgg ctg tcg gcg aag tat ccc 2906
Trp Val Pro Thr Glu Asp Glu Met Gly Trp Leu Ser Ala Lys Tyr Pro
            355   360   365

gac tcg ttc gac cgc tac tac cgc ccg cgc ttc gat cac tgg ggc gag 2954
Asp Ser Phe Asp Arg Tyr Tyr Arg Pro Arg Phe Asp His Trp Gly Glu
            370   375   380

cag gcc agg gcc ggc aac cgc ttc tac atg aag acg ctg ccg atg ctg 3002
Gln Ala Arg Ala Gly Asn Arg Phe Tyr Met Lys Thr Leu Pro Met Leu
385   390   395   400

tgc cag acg tgc cag atc ccg atg ctg ttc acc gag ccg ggc aac ccg 3050
Cys Gln Thr Cys Gln Ile Pro Met Leu Phe Thr Glu Pro Gly Asn Pro
            405   410   415

acg aag atc ggc gcg cgc gaa tcg aac tac ctc ggc aac aag ttc cac 3098
Thr Lys Ile Gly Ala Arg Glu Ser Asn Tyr Leu Gly Asn Lys Phe His
            420   425   430

ttc tgc agc gac cac tgc aag gac atc ttc gat cac gag ccg cag aaa 3146

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Phe Cys Ser Asp His Cys Lys Asp Ile Phe Asp His Glu Pro Gln Lys
            435             440             445

tac gtg cag gcg tgg ctg ccg gtg cac cag atc cat cag ggc aac tgc   3194
Tyr Val Gln Ala Trp Leu Pro Val His Gln Ile His Gln Gly Asn Cys
            450             455             460

ttc ccg ccc gat gcg gac ccg ggc gcg gag ggc ttc gat ccg ctc gcc   3242
Phe Pro Pro Asp Ala Asp Pro Gly Ala Glu Gly Phe Asp Pro Leu Ala
465             470             475             480

gcg gtg ctc gac tac tac gcg gtg acg atg ggc cgc gac aac ctc gat   3290
Ala Val Leu Asp Tyr Tyr Ala Val Thr Met Gly Arg Asp Asn Leu Asp
                485             490             495

ttc gac ggc tcg gaa gac cag aag aac ttc gcg gcg tgg cgc ggc cag   3338
Phe Asp Gly Ser Glu Asp Gln Lys Asn Phe Ala Ala Trp Arg Gly Gln
            500             505             510

gcc acg cgc aac                                                   3350
Ala Thr Arg Asn
            515

tgacccgcaa cgacaagcaa tcttgacgag ggcccgcgaa gcgccgatgc gcgaacgcgg 3410
gccgacagga gacaaac                                                3427

atg gcc gtc atc gcg ctc aaa ccc tac gac ttc ccg gtg aag gat gcc   3475
Met Ala Val Ile Ala Leu Lys Pro Tyr Asp Phe Pro Val Lys Asp Ala
                5               10              15

gtc gag aag ttt ccg gcg ccg ctg ctc tac gtg tgc tgg gaa aac cat   3523
Val Glu Lys Phe Pro Ala Pro Leu Leu Tyr Val Cys Trp Glu Asn His
            20              25              30

ctg atg ttc ccg gcg ccg ttc tgc ctg ccg ctg ccg ccc gac atg ccg   3571
Leu Met Phe Pro Ala Pro Phe Cys Leu Pro Leu Pro Pro Asp Met Pro
            35              40              45

ttc ggc gcg ctg gcc ggc gac gtg ctg ccg ccc gtc tac ggc tat cac   3619
Phe Gly Ala Leu Ala Gly Asp Val Leu Pro Pro Val Tyr Gly Tyr His
            50              55              60

ccc gac ttc gcg aag atc gac tgg gat cgc gtc gag tgg ttc cgg tcg   3667
Pro Asp Phe Ala Lys Ile Asp Trp Asp Arg Val Glu Trp Phe Arg Ser
65              70              75              80

ggc gag ccg tgg gcg ccg gac ccg gcg aag agc ctg gcc ggc aac ggc   3715
Gly Glu Pro Trp Ala Pro Asp Pro Ala Lys Ser Leu Ala Gly Asn Gly
            85              90              95
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ctc ggg cac aag gac ctg atc agc ttc cgc acg ccc ggc ctc gac ggc   3763

Leu Gly His Lys Asp Leu Ile Ser Phe Arg Thr Pro Gly Leu Asp gly

           100   105   110

ctc ggc ggc gcg agc ttc   3781

Leu Gly Gly Ala Ser Phe

        115

tgaccgccac gcggacgagc gaaccatc   3809

atg agc cac caa ctt acc atc gag ccg ctg ggc gtc acg atc gag gtc   3857

Met Ser His Gln Leu Thr Ile Glu Pro Leu Gly Val Thr Ile Glu Val

             5   10   15

gag gaa gga cag acg atg ctc gat gcc gcg ctg cgc cag ggc atc tac   3905

Glu Glu Gly Gln Thr Met Leu Asp Ala Ala Leu Arg Gln Gly Ile Tyr

           20   25   30

att ccg cac gcg tgc tgt cac ggg ctg tgc ggc acc tgc aag gtc gcc   3953

Ile Pro His Ala Cys Cys His Gly Leu Cys Gly Thr Cys Lys Val Ala

          35   40   45

gtg ctc gac ggc gag acc gat ccc ggc gat gcg aac ccg ttc gcg ctg   4001

Val Leu Asp Gly Glu Thr Asp Pro Gly Asp Ala Asn Pro Phe Ala Leu

          50   55   60

atg gat ttc gag cgc gag gaa ggc aag gcg ctc gcg tgc tgc gcg acg   4049

Met Asp Phe Glu Arg Glu Glu Gly Lys Ala Leu Ala Cys Cys Ala Thr

65   70   75   80

ctg cag gcc gac acc gtg atc gag gcc gac gtc gac gag gag ccg gat   4097

Leu Gln Ala Asp Thr Val Ile Glu Ala Asp Val Asp Glu Glu Pro Asp

           85   90   95

gcg gaa atc atc ccg gtc agg gat ttc gcg gcc gac gtc acg cgc atc   4145

Ala Glu Ile Ile Pro Val Arg Asp Phe Ala Ala Asp Val Thr Arg Ile

           100   105   110

gaa cag ctc acg ccg acc atc aag tcg atc cgc ctg aag ctg tcg cag   4193

Glu Gln Leu Thr Pro Thr Ile Lys Ser Ile Arg Leu Lys Leu Ser Gln

          115   120   125

ccg atc cgc ttc cag gcg ggc cag tac gtg cag ctc gag att ccc ggc   4241

Pro Ile Arg Phe Gln Ala Gly Gln Tyr Val Gln Leu Glu Ile Pro Gly

          130   135   140

ctc ggg cag agc cgc gcg ttc tcg atc gcg aac gcg ccg gcc gac gtc   4289

Leu Gly Gln Ser Arg Ala Phe Ser Ile Ala Asn Ala Pro Ala Asp Val

145   150   155   160

gcg gcc acc ggc gag atc gaa ctg aac gtg cgg cag gtg ccg ggc ggg   4337
Ala Ala Thr Gly Glu Ile Glu Leu Asn Val Arg Gln Val Pro Gly Gly
             165   170   175

ctc ggc acg ggc tac ctg cac gag caa ctg gcg acg ggc gag cgc gtg   4385
Leu Gly Thr Gly RTr Leu His Glu Gln Leu Ala Thr Gly Glu Arg Val
             180   185   190

cgc ctg tcg ggc ccg tac ggc cgc ttc ttc gtg cgt cgc tcg gcc gcg   4433
Arg Leu Ser Gly Pro Tyr Gly Arg Phe Phe Val Arg Arg Ser Ala Ala
             195   200   205

cgg ccg atg atc ttc atg gcc ggc ggg tcg ggg ctg tcg agc ccg cgc   4481
arg Pro Met Ile Phe Met ala gly gly Ser gly Leu Ser Ser Pro arg
             210   215   220

tcg atg atc gcg gac ctg ctc gca agc ggc gtc acc gcg ccg atc acg   4529
Ser Met Ile ala asp Leu Leu ala Ser gly Val thr ala Pro Ile thr
225   230   235   240

ctg gtc tac ggt cag cgc agc gcg cag gag ctc tac tac cac gac gaa   4577
Leu Val tyr gly gln arg Ser ala gln glu Leu tyr tyr His asp glu
             245   250   255

ttc cgc gcg ctg gcc gaa cgc cat ccg aac ttc acg tac gtg ccg gcg   4625
Phe arg ala Leu ala glu arg His Pro asn Phe thr tyr Val Pro ala
             260   265   270

ctg tcc gaa ggc gca ccg cac gcg ggc ggc gac gtc gcg caa ggg ttc   4673
Leu Ser Glu Gly Ala Pro His Ala Gly Gly Asp Val Ala Gln Gly Phe
             275   280   285

gtg cac gac gtc gcg aag gca cat ttc ggc ggc gac ttc tcc ggg cac   4721
Val His Asp Val Ala Lys Ala His Phe Gly Gly Asp Phe Ser Gly His
             290   295   300

cag gcg tac ctg tgc ggg ccg ccc gcg atg atc gac gcg tgc atc acg   4769
Gln Ala Tyr Leu Cys Gly Pro Pro Ala Met Ile Asp Ala Cys Ile Thr
305   310   315   320

acg ctg atg cag ggg cgc ctg ttc gag cgc gac atc tat cac gag aag   4817
Thr Leu Met Gln Gly Arg Leu Phe Glu Arg Asp Ile Tyr His Glu Lys
             325   330   335

ttc atc tcg gcg gcc gac gcg caa cag acg cgc agc ccg ctg ttc cgg   4865
Phe Ile Ser Ala Ala Asp Ala Gln Gln Thr Arg Ser Pro Leu Phe Arg
             340   345   350

cgg gtg   4871

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Arg Val

tgac                                                                    4875

atg gac gcg ggc cgc gta tgc ggg acg gtc acg atc gcg cag acc gac   4923
Met Asp Ala Gly Arg Val Cys Gly Thr Val Thr Ile Ala Gln Thr Asp
                5                   10                  15

gag cgc tat gcg tgc gtg tcc ggc gag tcg ctg ctg gcc ggc atg gcg   4971
Glu Arg Tyr Ala Cys Val Ser Gly Glu Ser Leu Leu Ala Gly Met Ala
                20                  25                  30

aaa ctc ggc cgg cgc ggc att ccg gtc ggc tgc ctg aac ggc ggg tgc   5019
Lys Leu Gly Arg Arg Gly Ile Pro Val Gly Cys Leu Asn Gly Gly Cys
                35                  40                  45

ggc gtg tgc aag gtg cgc gtg ctg cgc ggt gcg gtg cgc aag ctc ggg   5067
Gly Val Cys Lys Val Arg Val Leu Arg Gly Ala Val Arg Lys Leu Gly
            50                  55                  60

ccg atc agc cgt gcc cat gtg agc gcg gaa gaa gag aac gac ggc tac   5115
Pro Ile Ser Arg Ala His Val Ser Ala Glu Glu Glu Asn Asp Gly Tyr
65                  70                  75                  80

gcg ctt gcg tgc cgc gtc gtg ccg gac ggc gac gtc gaa ctc gaa gtg   5163
Ala Leu Ala Cys Arg Val Val Pro Asp Gly Asp Val Glu Leu Glu Val
                85                  90                  95

gcc ggc cgg ctc agg aag ccg ttc ttc tgc ggc atg gca tgt gcc ggc   5211
Ala Gly Arg Leu Arg Lys Pro Phe Phe Cys Gly Met Ala Cys Ala Gly
                100                 105                 110

acg gcg gcg atc aac aag                                            5229
Thr Ala Ala Ile Asn Lys
                115

taaccaggag gagactcacc atgggtgtga tgcgtattgg tcatgtcagt ctgaaggtga 5289
tggacatgga agcggcgctg cgtcattacg tacgcgtgct cggcatgcag gaaacgatgc 5349
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Met Glu Ala Thr Pro Ile Met Asn Gln His Pro Thr Asp Leu Ser Pro
                    5   10   15

Phe Asp Pro Gly Arg Lys Cys Val Arg Val Thr Gly Thr Asn Ala Arg
                    20   25   30

Gly Phe Val Glu Phe Glu Leu Ser Ile Gly Gly Ala Pro Glu Leu Cys
            35   40   45

Val Glu Leu Thr Leu Ser Pro Ala Ala Phe Asp Ala Phe Cys Arg Glu
        50   55   60

Gln Gln Val Thr Arg Leu Asp Val Glu Ala Asn Pro
65   70   75

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<213> Burkholderia cepacia

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<400> 3

Met Arg Ser Ala Ala Asn Ser Arg Ser Arg Gly Ser Thr Ser Lys Arg
                    5   10   15

Thr His Asp Leu Glu Glu Gln Glu Val Thr Ile Glu Leu Lys Thr Val
                    20   25   30

Asp Ile Lys Pro Leu Arg His Thr Phe Ala His Val Ala Gln Asn Ile
            35   40   45

Gly Gly Asp Lys Thr Ala Thr Arg Tyr Gln Glu Gly Met Met Gly Ala
        50   55   60

Gln Pro Gln Glu Asn Phe His Tyr Arg Pro Thr Trp Asp Pro Asp Tyr
65   70   75   80

Glu Ile Phe Asp Pro Ser Arg Ser Ala Ile Arg Met Ala Asn Trp Tyr
                    85   90   95

Ala Leu Lys Asp Pro Arg Gln Phe Tyr Tyr Ala Ser Trp Ala Thr Thr
                    100   105   110

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Arg Ala Arg Gln Gln Asp Ala Met Glu Ser Asn Phe Glu Phe Val Glu
        115                 120                 125

Ser Arg Arg Met Ile Gly Leu Met Arg Asp Asp Val Ala Ala Arg Ala
        130                 135                 140

Leu Asp Val Leu Val Pro Leu Arg His Ala Ala Trp Gly Ala Asn Met
145                 150                 155                 160

Asn Asn Ala Gln Ile Cys Ala Leu Gly Tyr Gly Thr Val Phe Thr Ala
                165                 170                 175

Pro Ala Met Phe His Ala Met Asp Asn Leu Gly Val Ala Gln Tyr Leu
                180                 185                 190

Thr Arg Leu Ala Leu Ala Met Ala Glu Pro Asp Val Leu Glu Ala Ala
        195                 200                 205

Lys Ala Thr Trp Thr Arg Asp Ala Ala Trp Gln Pro Leu Arg Arg Tyr
        210                 215                 220

Val Glu Asp Thr Leu Val Val Ala Asp Pro Val Glu Leu Phe Ile Ala
225                 230                 235                 240

Gln Asn Leu Ala Leu Asp Gly Leu Leu Tyr Pro Leu Val Tyr Asp Arg
                245                 250                 255

Phe Val Asp Glu Arg Ile Ala Leu Glu Gly Gly Ser Ala Val Ala Met
                260                 265                 270

Leu Thr Ala Phe Met Pro Glu Trp His Thr Glu Ser Asn Arg Trp Ile
        275                 280                 285

Asp Ala Val Val Lys Thr Met Ala Ala Glu Ser Asp Asp Asn Arg Ala
        290                 295                 300

Leu Leu Ala Arg Trp Thr Arg Asp Trp Ser Ala Arg Ala Glu Ala Ala
305                 310                 315                 320

Leu Ala Pro Val Ala Ala Arg Ala Leu Gln Asp Ala Gly Arg Ala Ala
                325                 330                 335

Leu Asp Glu Val Arg Glu Gln Phe His Ala Arg Ala Ala Arg Leu Gly
                340                 345                 350

Ile Ala Leu
        355

<210> 4

<211> 89

<212> PRT

<213> Burkholderia cepacia

<220>
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<223> TomM polypepetide

<400> 4

Met Ser Asn Val Phe Ile Ala Phe Gln Ala Asn Glu Asp Ser Arg Pro
                5   10   15

Ile Val Asp Ala Ile Val Ala Asp Asn Pro Arg Ala Val Val Val Glu
        20   25   30

Ser Pro Gly Met Val Lys Ile Asp Ala Pro Asp Arg Leu Thr Ile Arg
        35   40   45

Arg Glu Thr Ile Glu Glu Leu Thr Gly Thr Arg Phe Asp Leu Gln Gln
        50   55   60

Leu Gln Val Asn Leu Ile Thr Leu Ser Gly His Ile Asp Glu Asp Asp
65   70   75   80

Asp Glu Phe Thr Leu Ser Trp Ser His
                85

<210> 5

<211> 516

<212> PRT

<213> Burkholeria cepacia

<223> TomN polypeptide

<400> 5

Met Asp Thr Pro Thr Leu Lys Lys Lys Leu Gly Leu Lys Asp Arg Tyr
                5   10   15

Ala Ala Met Thr Arg Gly Leu Gly Trp Glu Thr Thr Tyr Gln Pro Met
        20   25   30

Asp Lys Val Phe Pro Tyr Asp Arg Tyr Glu Gly Ile Lys Ile His Asp
        35   40   45

Trp Asp Lys Trp Val Asp Pro Phe Arg Leu Thr Met Asp Ala Tyr Trp
        50   55   60

Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu Tyr Ala Val Ile Asp Ala
65   70   75   80

Phe Thr Gln Asn Asn Ala Phe Leu Gly Val Ser Asp Ala Arg Tyr Ile
                85   90   95

Asn Ala Leu Lys Leu Phe Leu Gln Gly Val Thr Pro Leu Glu Tyr Leu
                100   105   110

Ala His Arg Gly Phe Ala His Val Gly Arg His Phe Thr Gly Glu Gly
                115   120   125

Ala Arg Ile Ala Cys Gln Met Gln Ser Ile Asp Glu Leu Arg His Tyr

```
          130                   135                   140
Gln Thr Glu Thr His Ala Met Ser Thr Tyr Asn Lys Phe Phe Asn Gly
145                   150                   155                   160
Phe His His Ser Asn Gln Trp Phe Asp Arg Val Trp Tyr Leu Ser Val
                      165                   170                   175
Pro Lys Ser Phe Phe Glu Asp Ala Tyr Ser Ser Gly Pro Phe Glu Phe
                      180                   185                   190
Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu
                      195                   200                   205
Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr
          210                   215                   220
Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr
225                   230                   235                   240
Leu Gly Ile Glu Cys Ile Lys Phe Leu Leu Glu Gln Asp Pro Asp Asn
                      245                   250                   255
Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr
                      260                   265                   270
Arg Leu Leu Thr Leu Val Ala Met Met Met Asp Tyr Met Gln Pro Lys
                      275                   280                   285
Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Ala Glu Gln Asn
          290                   295                   300
Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg Tyr Gly Ile Arg Glu Pro
305                   310                   315                   320
Lys Gly Trp Gln Asp Ala Cys Glu Gly Lys Asp His Ile Ser His Gln
                      325                   330                   335
Ala Trp Ser Thr Phe Tyr Gly Phe Asn Ala Ala Ser Ala Phe His Thr
                      340                   345                   350
Trp Val Pro Thr Glu Asp Glu Met Gly Trp Leu Ser Ala Lys Tyr Pro
                      355                   360                   365
Asp Ser Phe Asp Arg Tyr Tyr Arg Pro Arg Phe Asp His Trp Gly Glu
          370                   375                   380
Gln Ala Arg Ala Gly Asn Arg Phe Tyr Met Lys Thr Leu Pro Met Leu
385                   390                   395                   400
Cys Gln Thr Cys Gln Ile Pro Met Leu Phe Thr Glu Pro Gly Asn Pro
                      405                   410                   415
Thr Lys Ile Gly Ala Arg Glu Ser Asn Tyr Leu Gly Asn Lys Phe His
                      420                   425                   430
```

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Phe Cys Ser Asp His Cys Lys Asp Ile Phe Asp His Glu Pro Gln Lys
        435             440             445
Tyr Val Gln Ala Trp Leu Pro Val His Gln Ile His Gln Gly Asn Cys
    450             455             460
Phe Pro Pro Asp Ala Asp Pro Gly Ala Glu Gly Phe Asp Pro Leu Ala
465             470             475             480
Ala Val Leu Asp Tyr Tyr Ala Val Thr Met Gly Arg Asp Asn Leu Asp
            485             490             495
Phe Asp Gly Ser Glu Asp Gln Lys Asn Phe Ala Ala Trp Arg Gly Gln
            500             505             510
Ala Thr Arg Asn
        515
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<210> 6

<211> 118

<212> PRT

<213> Burkholderia cepacia

<220>

<223> TomO polypeptide

<400> 6

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Met Ala Val Ile Ala Leu Lys Pro Tyr Asp Phe Pro Val Lys Asp Ala
                5               10              15
Val Glu Lys Phe Pro Ala Pro Leu Leu Tyr Val Cys Trp Glu Asn His
            20              25              30
Leu Met Phe Pro Ala Pro Phe Cys Leu Pro Leu Pro Pro Asp Met Pro
            35              40              45
Phe Gly Ala Leu Ala Gly Asp Val Leu Pro Pro Val Tyr Gly Tyr His
    50              55              60
Pro Asp Phe Ala Lys Ile Asp Trp Asp Arg Val Glu Trp Phe Arg Ser
65              70              75              80
Gly Glu Pro Trp Ala Pro Asp Pro Ala Lys Ser Leu Ala Gly Asn Gly
            85              90              95
Leu Gly His Lys Asp Leu Ile Ser Phe Arg Thr Pro Gly Leu Asp Gly
            100             105             110
Leu Gly Gly Ala Ser Phe
        115
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<210> 7

<211> 352

<212> PRT

<213> Burkholderia cepacia

<220>

<223> TomP polypeptide

<400> 7

Met Ser His Gln Leu Thr Ile Glu Pro Leu Gly Val Thr Ile Glu Val
                5   10   15

Glu Glu Gly Gln Thr Met Leu Asp Ala Ala Leu Arg Gin Gly Ile Tyr
            20   25   30

Ile Pro His Ala Cys Cys His Gly Leu Cys Gly Thr Cys Lys Val Ala
        35   40   45

Val Leu Asp Gly Glu Thr Asp Pro Gly Asp Ala Asn Pro Phe Ala Leu
        50   55   60

Met Asp Phe Glu Arg Glu Glu Gly Lys Ala Leu Ala Cys Cys Ala Thr
65   70   75   80

Leu Gln Ala Asp Thr Val Ile Glu Ala Asp Val Asp Glu Glu Pro Asp
                85   90   95

Ala Glu Ile Ile Pro Val Arg Asp Phe Ala Ala Asp Val Thr Arg Ile
            100   105   110

Glu Gln Leu Thr Pro Thr Ile Lys Ser Ile Arg Leu Lys Leu Ser Gln
            115   120   125

Pro Ile Arg Phe Gln Ala Gly Gln Tyr Val Gln Leu Glu Ile Pro Gly
        130   135   140

Leu Gly Gln Ser Arg Ala Phe Ser Ile Ala Asn Ala Pro Ala Asp Val
145   150   155   160

Ala Ala Thr Gly Glu Ile Glu Leu Asn Val Arg Gln Val Pro Gly Gly
                165   170   175

Leu Gly Thr Gly Tyr Leu His Glu Gln Leu Ala Thr Gly Glu Arg Val
            180   185   190

Arg Leu Ser Gly Pro Tyr Gly Arg Phe Phe Val Arg Arg Ser Ala Ala
            195   200   205

Arg Pro Met Ile Phe Met Ala Gly Gly Ser Gly Leu Ser Ser Pro Arg
        210   215   220

Ser Met Ile Ala Asp Leu Leu Ala Ser Gly Val Thr Ala Pro Ile Thr
225   230   235   240

Leu Val Tyr Gly Gln Arg Ser Ala Gln Glu Leu Tyr Tyr His Asp Glu
            245   250   255

Phe Arg Ala Leu Ala Glu Arg His Pro Asn Phe Thr Tyr Val Pro Ala
                260   265   270

Leu Ser Glu Gly Ala Pro His Ala Gly Gly Asp Val Ala Gln Gly Phe
            275   280   285

Val His Asp Val Ala Lys Ala His Phe Gly Gly Asp Phe Ser Gly His
        290   295   300

Gln Ala Tyr Leu Cys Gly Pro Pro Ala Met Ile Asp Ala Cys Ile Thr
305   310   315   320

Thr Leu Met Gln Gly Arg Leu Phe Glu Arg Asp Ile Tyr His Glu Lys
                325   330   335

Phe Ile Ser Ala Ala Asp Ala Gln Gln Thr Arg Ser Pro Leu Phe Arg
                340   345   350

<210> 8

<211> 118

<212> PRT

<213> Burkholderia cepacia

<220>

<223> TomQ polypeptide

<400> 8

Met Asp Ala Gly Arg Val Cys Gly Thr Val Thr Ile Ala Gln Thr Asp
                5   10   15

Glu Arg Tyr Ala Cys Val Ser Gly Glu Ser Leu Leu Ala Gly Met Ala
            20   25   30

Lys Leu Gly Arg Arg Gly Ile Pro Val Gly Cys Leu Asn Gly Gly Cys
            35   40   45

Gly Val Cys Lys Val Arg Val Leu Arg Gly Ala Val Arg Lys Leu Gly
        50   55   60

Pro Ile Ser Arg Ala His Val Ser Ala Glu Glu Glu Asn Asp Gly Tyr
65   70   75   80

Ala Leu Ala Cys Arg Val Val Pro Asp Gly Asp Val Glu Leu Glu Val
            85   90   95

Ala Gly Arg Leu Arg Lys Pro Phe Phe Cys Gly Met Ala Cys Ala Gly
            100   105   110

Thr Ala Ala Ile Asn Lys
            115

<210> 9

<211> 36

<212> DNA

<213> Artificial Sequence

<223> Designed PCR primer

<400> 9

agtccgccat ggaggcgaca ccgatcatga atcagc 36

<210> 10

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed PCR Primer

<400> 10

caccgaccat ggatcagcac cccaccgatc tttc   34

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

<223> Designed PCR primer

<400> 11

tgccgccttc catgggttct gccgcgaaca gcag   34

<210> 12

<211> 39

<212> DNA

<220>

<213> Artificial Sequence

<223> Designed PCR primer

<400> 12

agcaagccat ggccatcgag ctgaagacag tcgacatca   39

<210> 13

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed PCR primer

<400> 13

ccgaccatca cctgctcggc cagatggaag tcgag   35